



PCT

RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/510,162

TIME: 12:04:13

Input Set : A:\38509-0016US1.txt

Output Set: N:\CRF4\10122004\J510162.raw

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3 <110> APPLICANT: Corena T. McMANUS
4   David A. JONES
6 <120> TITLE OF INVENTION: METHYL-CPG BINDING DOMAIN PROTEIN 2 HOMOLOGS
8 <130> FILE REFERENCE: 38509-0016US1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/510,162
C--> 11 <141> CURRENT FILING DATE: 2004-10-05
13 <150> PRIOR APPLICATION NUMBER: PCT/US03/10631
14 <151> PRIOR FILING DATE: 2003-04-07
16 <150> PRIOR APPLICATION NUMBER: 60/369,851
17 <151> PRIOR FILING DATE: 2002-04-05
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 812
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 ctttacagaa gaaacgagaa atccacatgg ccaaggccca tcggagacga gctgcgaggt 180
32 ctgctctccc catgagactc accagctgca tcttccggag gccggtgaca aggatcaggt 240
33 ctcacacctga caaccagggtc agacgcagaa aaggggacga gcacctggag aagccgcagc 300
34 aactctgcgc ctaccggaga ctgcaggccc tgcagccctg cagcagccaa ggagaaggtt 360
35 caagtccact gcatttggag agcgtcttaa gtatccttgc accgggggacg gccagtgaat 420
36 ctctggacag ggctggtgct gacgctgtgc gcagcccgtg tgagcccacc cctgggcggt 480
37 ttccagctgt ggcagggggg ccaacccagc gaatgggttg tcagctccca ccgcccctct 540
38 ctggccaatt ggtgactcct gcagatatcc ggagacaggc caggaggggtg aagaaagcca 600
39 gggagagact ggccaaggcc ttgcaggcag acaggctggc caggcaggca gaaatgctga 660
40 catgtagatg aagcgcagtc ctgggctttc ggccctttc ttttaatgcc catcctcatt 720
41 cctactctga attgtcacac ttttcccttc cccaccagtt ctttaataaa agtatttgaa 780
42 aggcacaaaa aaaaaaaaaa aaaaaaagat tt 812
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46 <211> LENGTH: 208
47 <212> TYPE: PRT
48 <213> ORGANISM: Homo sapiens
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54 Lys Leu Lys Arg Asn Met Met Pro Trp Ala Leu Gln Lys Lys Arg Glu
55           20           25           30
57 Ile His Met Ala Lys Ala His Arg Arg Arg Ala Ala Arg Ser Ala Leu
58           35           40           45
60 Pro Met Arg Leu Thr Ser Cys Ile Phe Arg Arg Pro Val Thr Arg Ile

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61      50      55      60
63 Arg Ser His Pro Asp Asn Gln Val Arg Arg Arg Lys Gly Asp Glu His
64 65      70      75      80
66 Leu Glu Lys Pro Gln Gln Leu Cys Ala Tyr Arg Arg Leu Gln Ala Leu
67      85      90      95
69 Gln Pro Cys Ser Ser Gln Gly Glu Gly Ser Ser Pro Leu His Leu Glu
70      100      105      110
72 Ser Val Leu Ser Ile Leu Ala Pro Gly Thr Ala Ser Glu Ser Leu Asp
73      115      120      125
75 Arg Ala Gly Ala Glu Arg Val Arg Ser Pro Leu Glu Pro Thr Pro Gly
76      130      135      140
78 Arg Phe Pro Ala Val Ala Gly Gly Pro Thr Pro Gly Met Gly Cys Gln
79 145      150      155      160
81 Leu Pro Pro Pro Leu Ser Gly Gln Leu Val Thr Pro Ala Asp Ile Arg
82      165      170      175
84 Arg Gln Ala Arg Arg Val Lys Lys Ala Arg Glu Arg Leu Ala Lys Ala
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87 Leu Gln Ala Asp Arg Leu Ala Arg Gln Ala Glu Met Leu Thr Cys Arg
88      195      200      205
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92 <211> LENGTH: 790
93 <212> TYPE: DNA
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99 agttcacaga ggaagcaacg tgactgtgta aaccaatgca aatcaaagcc tggcttgagc 180
100 acctcaatcc ctttgagaat gtccagttac acattcaaga ggccagtaac gagaattaca 240
101 ccccatcctg gcaatgaggt cagataccat caatgggagg agagcttgga gaagcctcag 300
102 caggtctgct ggcagaggag actgcaggga ctccaggctt acagcagtgc aggagaactt 360
103 tcaagcactt tggatcttgc caataccttg caaaaacttg tccctagtta cacaggtgga 420
104 tctctgctgg aggatcttgc cagtggctct gagcactcct gccccatgcc ccaccttgcc 480
105 tgctcttcag atgcggtgga gataattcct gcagagggag tgggtatctc gcagctcctc 540
106 tgcaaacaat ttctggtcac tgaggaagat atcaggaaac aggaagggaa agtgaagaca 600
107 gtcagagaga gactcgcaat agcactgatt gcggatggac tcgctaata gaagcagagaaa 660
108 gtgagagacc aagaaggctg tcctgaaaaa cgctaagaaa aaaagggaa atagtgcaga 720
109 tgaaataaag tgtaatcctt tattaacatc tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780
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114 <211> LENGTH: 194
115 <212> TYPE: PRT
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122 Lys Ser Lys Pro Gly Leu Ser Thr Ser Ile Pro Leu Arg Met Ser Ser
123      20      25      30
125 Tyr Thr Phe Lys Arg Pro Val Thr Arg Ile Thr Pro His Pro Gly Asn
126      35      40      45

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128 Glu Val Arg Tyr His Gln Trp Glu Glu Ser Leu Glu Lys Pro Gln Gln
129      50              55              60
131 Val Cys Trp Gln Arg Arg Leu Gln Gly Leu Gln Ala Tyr Ser Ser Ala
132 65              70              75              80
134 Gly Glu Leu Ser Ser Thr Leu Asp Leu Ala Asn Thr Leu Gln Lys Leu
135              85              90              95
137 Val Pro Ser Tyr Thr Gly Gly Ser Leu Leu Glu Asp Leu Ala Ser Gly
138              100              105              110
140 Leu Glu His Ser Cys Pro Met Pro His Leu Ala Cys Ser Ser Asp Ala
141              115              120              125
143 Val Glu Ile Ile Pro Ala Glu Gly Val Gly Ile Ser Gln Leu Leu Cys
144      130              135              140
146 Lys Gln Phe Leu Val Thr Glu Glu Asp Ile Arg Lys Gln Glu Gly Lys
147 145              150              155              160
149 Val Lys Thr Val Arg Glu Arg Leu Ala Ile Ala Leu Ile Ala Asp Gly
150              165              170              175
152 Leu Ala Asn Glu Ala Glu Lys Val Arg Asp Gln Glu Gly Cys Pro Glu
153              180              185              190
155 Lys Arg
158 <210> SEQ ID NO: 5
159 <211> LENGTH: 262
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 5
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167 Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser
168              20              25              30
170 Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
171              35              40              45
173 Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
174      50              55              60
176 Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
177 65              70              75              80
179 Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
180              85              90              95
182 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
183              100              105              110
185 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
186              115              120              125
188 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
189      130              135              140
191 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
192 145              150              155              160
194 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
195              165              170              175
197 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
198              180              185              190
200 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro

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201          195          200          205
203 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
204          210          215          220
206 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
207 225          230          235          240
209 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
210          245          250          255
212 Asp Ser Gly Asp Glu Ala
213          260
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 291
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 6
222 Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
223 1          5          10          15
225 Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
226          20          25          30
228 Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
229          35          40          45
231 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
232          50          55          60
234 Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
235          65          70          75          80
237 Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
238          85          90          95
240 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
241          100          105          110
243 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
244          115          120          125
246 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
247          130          135          140
249 Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
250          145          150          155          160
252 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
253          165          170          175
255 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
256          180          185          190
258 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
259          195          200          205
261 Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
262          210          215          220
264 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
265          225          230          235          240
267 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
268          245          250          255
270 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
271          260          265          270
273 Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met

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274	275	280	285
276	Glu His Val		
277	290		

VERIFICATION SUMMARY

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Input Set : A:\38509-0016US1.txt

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date